<110> Eli Lilly and Company

Beals, John

<120> ERYTHROPOIETIC COMPOUNDS

<130> X-12553

<140> US 09/856,451

<141> 2001-05-22

<150> PCT/US99/27801

<151> 1999-11-23

<160> 4

<170> PatentIn version 3.0

<210> 1

<211> 168

<212> PRT

<213> synthetic construct

<220>

<221> VARIANT

<222> (1)..(1)

<223> Xaa at position 1 is absent or Met;

<220>

<221> VARIANT

<222> (2)..(2)

<223> Xaa at position 2 is absent or is Ala, Cys, Asp, Glu, Phe, Gly, His Ile, Leu, Met, Asn, Gln, Arg, Ser, Thr, Val, Trp, or Tyr

<220>

<221> VARIANT

<222> (26)..(26)

<223> Xaa at position 26 is Asn, Lys or Glu;

<220>

<221> VARIANT

<222> (40)..(40)

<223> Xaa at position 40 is Asn, Lys or Glu;

<220>

<221> VARIANT

<222> (78)..(78)

<223> Xaa at position 78 is Arg or Glu;

<220>

<221> VARIANT

<222> (85)..(85)

<223> Xaa at position 85 is Asn, Lys or Glu;

<220>

<221> VARIANT

<222> (90)..(90)

<223> Xaa at position 90 is Trp, Lys, Pro, or Arg;

<220>

<221> VARIANT

<222> (128)..(128)

<223> Xaa at position 128 is Ser, Thr, Lys or Glu;

<220>

<221> VARIANT

<222> (141)..(141)

<223> Xaa at position 141 is Arg or Glu;

<220>

<221> VARIANT

<222> (156)..(156)

<223> Xaa at position 156 is Lys or Glu; and

<220>

<221> VARIANT

<222> (168)..(168)

<223> Xaa at position 168 is Arg, absent, or any other amino acid.

<400> 1

Xaa Xaa Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg
1 5 10 15

Tyr Leu Leu Glu Ala Lys Glu Ala Glu Xaa Ile Thr Thr Gly Cys Ala
20 25 30

Glu His Cys Ser Leu Asn Glu Xaa Ile Thr Val Pro Asp Thr Lys Val
35 40 45

Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu
50 55 60

Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Xaa Gly Gln
65 70 75 80

Ala Leu Leu Val Xaa Ser Ser Gln Pro Xaa Glu Pro Leu Gln Leu His
85 90 95

Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg
100 105 110

Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Xaa
115 120 125

Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Xaa Lys Leu Phe
130 135 140

Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Xaa Leu Tyr Thr Gly
145 150 155 160

Glu Ala Cys Arg Thr Gly Asp Xaa
165

<210> 2

<211> 193

<212> PRT

<213> Homo sapiens

<400> 2

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
1 5 10 15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
20 25 30

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
35 40 45

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
50 55 60

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
65 70 75 80

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
85 90 95

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
100 105 110

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
115 120 125

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
130 135 140

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
145 150 155 160

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
165 170 175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
180 185 190

Arg

<210> 3

<211> 498

<212> DNA

<213> synthetic construct

<220>

<221> CDS

<222> (1)..(495)

<400> 3

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gct cca cca cgt ctt att tgt gat tct cgt gtt ctt gaa cgt tac ctg
 48
Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu

1               5                  10                  15

ctg gaa gct aaa gaa gct gaa aac atc acc acc ggt tgc gct gaa cac
 96
Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His

            20                  25                  30

tgc tcc ctg aac gaa aac atc acc gtt ccg gac acc aaa gtt aac ttc
144
Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe

        35                  40                  45

tac gct tgg aaa cgt atg gaa gtt ggt cag cag gct gtt gaa gtt tgg
192
Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp

    50                  55                  60

cag ggt ctg gct ctg ctg tcc gaa gct gtt ctg cgt ggt cag gct ctg
240
Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu

65                  70                  75                  80

ctg gtt aac tcc tcc cag ccg tgg gaa ccg ctg cag ctg cac gtt gac
288
Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp

                85                  90                  95
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aaa gct gtt tcc ggt ctg cgt tcc ctg acc acc ctg ctg cgt gct ctg
336
Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu

            100                 105                 110


ggt gct cag aaa gaa gct atc tcc ccg ccg gac gct gct tcc gct gct
384
Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala

        115                 120                 125


ccg ctg cgt acc atc acc gct gac acc ttc cgt aaa ctg ttc cgt gtt
432
Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val

    130                 135                 140


tac tcc aac ttc ctg cgt ggt aaa ctg aaa ctg tac acc ggt gaa gct
480
Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala

145                 150                 155                 160


tgc cgt acc ggt gac tga
498
Cys Arg Thr Gly Asp

                165
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<210> 4

<211> 165

<212> PRT

<213> synthetic construct

<400> 4

Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu

1 5 10 15

Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His
20 25 30

Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe
35 40 45

Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp
50 55 60

Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
65 70 75 80

Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
85 90 95

Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
100 105 110

Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
115 120 125

Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
130 135 140

Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala
145 150 155 160

Cys Arg Thr Gly Asp
165